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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/925,637

DATE: 08/17/2001
TIME: 12:10:26

Input Set : A:\pb560-sl.txt
Output Set: N:\CRF3\08162001\I925637.raw

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3 <110> APPLICANT: Choi
5 <120> TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides
7 <130> FILE REFERENCE: PB560
9 <140> CURRENT APPLICATION NUMBER: US/09/925,637
9 <141> CURRENT FILING DATE: 2001-08-10
9 <150> PRIOR APPLICATION NUMBER: PCT/USQ0/23773
10 <151> PRIOR FILING DATE: 2000-08-31
12 <150> PRIOR APPLICATION NUMBER: US 60/151,933
13 <151> PRIOR FILING DATE: 1999-09-01
15 <150> PRIOR APPLICATION NUMBER: US 08/781,986
16 <151> PRIOR FILING DATE: 1997-01-03
18 <150> PRIOR APPLICATION NUMBER: US 08/956,171
19 <151> PRIOR FILING DATE: 1997-10-20
21 <150> PRIOR APPLICATION NUMBER: US 60/009,861
22 <151> PRIOR FILING DATE: 1996-01-06
24 <160> NUMBER OF SEQ ID NOS: 74
26 <170> SOFTWARE: PatentIn Ver. 2.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 1318
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
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35 atgcatgatt taggacatga agttcaagga tcggatattg agaactacgt atttacagaa 120
36 gttgctctta gaaataagg gataaaaata ttaccatttg atgctaataa cataaaagaa 180
37 gatatggtag ttatacaagg taatgcattc gcgagtagcc atgaagaaat agtacgtgca 240
38 catcaattga aattagatgt tgtaagttat aatgattttt taggacagat tattgatcaa 300
39 tatacttcag tagctgtaac tgggtgcacat ggtaaaactt ctacaacagg tttattatca 360
40 catgttatga atggtgataa aaagacttca tttttaattg gtgatggcac aggtatggga 420
41 ttgcttgaaa gtgattatgt cgcttttgag gcatgtgaat atagacgtca ctttttaagt 480
42 tataaacctg attacgcaat tatgacaaat attgatttcg atcatcctga ttattttaaa 540
43 gatattaatg atgtttttga tgcattccaa gaaatggcac ataattgtta aaaaggatt 600
44 attgcttggg gtgatgatga acatctacgt aaaattgaag cagatgttcc aatttattat 660
45 tatggattta aagattcgga tgacatttat gctcaaaata ttcaaattac ggataaagg 720
46 actgcttttg atgtgtatgt ggatggtgag ttttatgatc acttcctgtc tccacaatat 780
47 ggtgaccata cagtttttaa tgcattagct gtaattgcca ttagttattt agagaagcta 840
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49 gaaactacaa ttgcaaatca agttattgta gatgattatg cacaccatcc aagagaaatt 960
50 agtgctacaa ttgaaacagc acgaaagaaa tatccacata aagaagttgt tgcagtattt 1020
51 caaccacaca ctttctctag aacacaggca tttttaaatg aatttgcaga aagttaaagt 1080
52 aaagcagatc gtgtattctt atgtgaaatt tttggatcaa ttagagaaaa tactggcgca 1140
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58 <211> LENGTH: 437
59 <212> TYPE: PRT

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p. 5

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67           20           25           30
69 Ile Glu Asn Tyr Val Phe Thr Glu Val Ala Leu Arg Asn Lys Gly Ile
70           35           40           45
72 Lys Ile Leu Pro Phe Asp Ala Asn Asn Ile Lys Glu Asp Met Val Val
73           50           55           60
75 Ile Gln Gly Asn Ala Phe Ala Ser Ser His Glu Glu Ile Val Arg Ala
76   65           70           75           80
78 His Gln Leu Lys Leu Asp Val Val Ser Tyr Asn Asp Phe Leu Gly Gln
79           85           90           95
81 Ile Ile Asp Gln Tyr Thr Ser Val Ala Val Thr Gly Ala His Gly Lys
82           100          105          110
84 Thr Ser Thr Thr Gly Leu Leu Ser His Val Met Asn Gly Asp Lys Lys
85           115          120          125
87 Thr Ser Phe Leu Ile Gly Asp Gly Thr Gly Met Gly Leu Pro Glu Ser
88           130          135          140
90 Asp Tyr Phe Ala Phe Glu Ala Cys Glu Tyr Arg Arg His Phe Leu Ser
91 145           150          155          160
93 Tyr Lys Pro Asp Tyr Ala Ile Met Thr Asn Ile Asp Phe Asp His Pro
94           165          170          175
96 Asp Tyr Phe Lys Asp Ile Asn Asp Val Phe Asp Ala Phe Gln Glu Met
97           180          185          190
99 Ala His Asn Val Lys Lys Gly Ile Ile Ala Trp Gly Asp Asp Glu His
100          195          200          205
102 Leu Arg Lys Ile Glu Ala Asp Val Pro Ile Tyr Tyr Tyr Gly Phe Lys
103          210          215          220
105 Asp Ser Asp Asp Ile Tyr Ala Gln Asn Ile Gln Ile Thr Asp Lys Gly
106 225          230          235          240
108 Thr Ala Phe Asp Val Tyr Val Asp Gly Glu Phe Tyr Asp His Phe Leu
109          245          250          255
111 Ser Pro Gln Tyr Gly Asp His Thr Val Leu Asn Ala Leu Ala Val Ile
112          260          265          270
114 Ala Ile Ser Tyr Leu Glu Lys Leu Asp Val Thr Asn Ile Lys Glu Ala
115          275          280          285
117 Leu Glu Thr Phe Gly Gly Val Lys Arg Arg Phe Asn Glu Thr Thr Ile
118          290          295          300
120 Ala Asn Gln Val Ile Val Asp Asp Tyr Ala His His Pro Arg Glu Ile
121 305          310          315          320
123 Ser Ala Thr Ile Glu Thr Ala Arg Lys Lys Tyr Pro His Lys Glu Val
124          325          330          335
126 Val Ala Val Phe Gln Pro His Thr Phe Ser Arg Thr Gln Ala Phe Leu
127          340          345          350
129 Asn Glu Phe Ala Glu Ser Leu Ser Lys Ala Asp Arg Val Phe Leu Cys
130          355          360          365
132 Glu Ile Phe Gly Ser Ile Arg Glu Asn Thr Gly Ala Leu Thr Ile Gln

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133      370      375      380
135 Asp Leu Ile Asp Lys Ile Glu Gly Ala Ser Leu Ile Asn Glu Asp Ser
136 385      390      395      400
138 Ile Asn Val Leu Glu Gln Phe Asp Asn Ala Val Ile Leu Phe Met Gly
139      405      410      415
141 Ala Gly Asp Ile Gln Lys Leu Gln Asn Ala Tyr Leu Asp Lys Leu Gly
142      420      425      430
144 Met Lys Asn Ala Phe
145      435
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150 <212> TYPE: DNA
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153 <400> SEQUENCE: 3
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156 gatttacaaa aaactgtaga tgtttatcgt aactataaag ctaaaaaaga agaattagct 180
157 gatattgaag aaatgttaag tgagactgat gataaagaag aagtagaaat gttaaaagag 240
158 gagagtaatg gtattaaagc tgaacttcca aatcttgaag aagagcttaa aatattattg 300
159 attcctaaag atcctaatag tgacaaagac gttattgtag aaataagagc agcagcaggt 360
160 ggtgatgagg ctgcgatttt tgctggtgat ttaatgcgta tgtattcaaa gtatgctgaa 420
161 tcacaaggat tcaaaactga aatagtagaa gcgtctgaaa gtgaccatgg tggttacaaa 480
162 gaaattagtt tctcagtttc tggtaatggc gcgtatagta aattgaaatt tgaaaatggt 540
163 gcgcaccgcg ttcaacgtgt gcctgaaaca gaatcaggtg gacgtattca tacttcaaca 600
164 gctacagtgg cagttttacc agaagttgaa gatgtagaaa ttgaaattag aaatgaagat 660
165 ttaaaaatcg acacgtatcg ttcaagtggg gcaggtgggc agcacgtaaa cacaactgac 720
166 tctgcagtac gtattaccca ttaccaact ggtgtcattg caacatcttc tgagaagtct 780
167 caaattcaaa accgtgaaaa agcaatgaaa gtgttaaaag cacgtttata cgatatgaaa 840
168 gttcaagaag aacaacaaaa gtatgcgtca caacgtaaat cagcagtcgg tactggtgat 900
169 cgttcagaac gtattcgaac ttataattat ccacaaagcc gtgtaacaga ccatcgtata 960
170 ggtctaacgc ttcaaaaatt agggcaaatt atggaaggcc atttagaaga aattatagat 1020
171 gcaactgactt tatcagagca gacagataaa ttgaaagaac ttaataatgg tgaa 1074
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175 <212> TYPE: PRT
176 <213> ORGANISM: Homo sapiens
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183      20      25      30
185 Arg Lys Tyr Ser Lys Glu Gln Ala Asp Leu Gln Lys Thr Val Asp Val
186      35      40      45
188 Tyr Arg Asn Tyr Lys Ala Lys Lys Glu Glu Leu Ala Asp Ile Glu Glu
189      50      55      60
191 Met Leu Ser Glu Thr Asp Asp Lys Glu Glu Val Glu Met Leu Lys Glu
192 65      70      75      80
194 Glu Ser Asn Gly Ile Lys Ala Glu Leu Pro Asn Leu Glu Glu Glu Leu
195      85      90      95

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197 Lys Ile Leu Leu Ile Pro Lys Asp Pro Asn Asp Asp Lys Asp Val Ile
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200 Val Glu Ile Arg Ala Ala Ala Gly Gly Asp Glu Ala Ala Ile Phe Ala
201           115           120           125
203 Gly Asp Leu Met Arg Met Tyr Ser Lys Tyr Ala Glu Ser Gln Gly Phe
204           130           135           140
206 Lys Thr Glu Ile Val Glu Ala Ser Glu Ser Asp His Gly Gly Tyr Lys
207 145           150           155           160
209 Glu Ile Ser Phe Ser Val Ser Gly Asn Gly Ala Tyr Ser Lys Leu Lys
210           165           170           175
212 Phe Glu Asn Gly Ala His Arg Val Gln Arg Val Pro Glu Thr Glu Ser
213           180           185           190
215 Gly Gly Arg Ile His Thr Ser Thr Ala Thr Val Ala Val Leu Pro Glu
216           195           200           205
218 Val Glu Asp Val Glu Ile Glu Ile Arg Asn Glu Asp Leu Lys Ile Asp
219           210           215           220
221 Thr Tyr Arg Ser Ser Gly Ala Gly Gly Gln His Val Asn Thr Thr Asp
222 225           230           235           240
224 Ser Ala Val Arg Ile Thr His Leu Pro Thr Gly Val Ile Ala Thr Ser
225           245           250           255
227 Ser Glu Lys Ser Gln Ile Gln Asn Arg Glu Lys Ala Met Lys Val Leu
228           260           265           270
230 Lys Ala Arg Leu Tyr Asp Met Lys Val Gln Glu Glu Gln Gln Lys Tyr
231           275           280           285
233 Ala Ser Gln Arg Lys Ser Ala Val Gly Thr Gly Asp Arg Ser Glu Arg
234           290           295           300
236 Ile Arg Thr Tyr Asn Tyr Pro Gln Ser Arg Val Thr Asp His Arg Ile
237 305           310           315           320
239 Gly Leu Thr Leu Gln Lys Leu Gly Gln Ile Met Glu Gly His Leu Glu
240           325           330           335
242 Glu Ile Ile Asp Ala Leu Thr Leu Ser Glu Gln Thr Asp Lys Leu Lys
243           340           345           350
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250 <211> LENGTH: 555

251 <212> TYPE: DNA

252 <213> ORGANISM: Homo sapiens

254 <400> SEQUENCE: 5

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257 acagttgatt actatggtgc accaacacct gtacaacaat tagcaagcat caatgttcca 180
258 gaagcacgtt tacttgttat ttctccatac gacaaaactt ctgtagctga catcgaaaaa 240
259 gcgataatag cagctaactt aggtgttaac ccaacaagtg atggtgaagt gatacgtatt 300
260 gctgtacctg ccttaacaga agaacgtaga aaagagcgcg ttaaagatgt taagaaaatt 360
261 ggtgaagaag ctaaagtatc tgttcgaaat attcgtcgtg atatgaatga tcagttgaaa 420
262 aaagatgaaa aaaatggcga cattactgaa gatgagttga gaagtggcac tgaagatgtt 480
263 cagaaagcaa cagacaattc aataaaagaa attgatcaaa tgattgctga taaagaaaaa 540
264 gatattatgt cagta                                     555

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Input Set : A:\pb560-sl.txt

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268 <212> TYPE: PRT
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276           20           25           30
278 Asn Ser Asn Leu Leu Asn Gly Val Thr Val Asp Tyr Tyr Gly Ala Pro
279           35           40           45
281 Thr Pro Val Gln Gln Leu Ala Ser Ile Asn Val Pro Glu Ala Arg Leu
282           50           55           60
284 Leu Val Ile Ser Pro Tyr Asp Lys Thr Ser Val Ala Asp Ile Glu Lys
285           65           70           75           80
287 Ala Ile Ile Ala Ala Asn Leu Gly Val Asn Pro Thr Ser Asp Gly Glu
288           85           90           95
290 Val Ile Arg Ile Ala Val Pro Ala Leu Thr Glu Glu Arg Arg Lys Glu
291           100          105          110
293 Arg Val Lys Asp Val Lys Lys Ile Gly Glu Glu Ala Lys Val Ser Val
294           115          120          125
296 Arg Asn Ile Arg Arg Asp Met Asn Asp Gln Leu Lys Lys Asp Glu Lys
297           130          135          140
299 Asn Gly Asp Ile Thr Glu Asp Glu Leu Arg Ser Gly Thr Glu Asp Val
300          145          150          155          160
302 Gln Lys Ala Thr Asp Asn Ser Ile Lys Glu Ile Asp Gln Met Ile Ala
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306           180          185
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310 <211> LENGTH: 1176
311 <212> TYPE: DNA
312 <213> ORGANISM: Homo sapiens
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317 tatgatagtg caagaaatgt ccgtgtggaa ttaaatatgg atcaaggtac tttcaaagtt 180
318 atcgctcgta aagatgttgt tgaagaagta tttgacgaca gagatgaagt ggatttaagt 240
319 acagcgcttg ttaaaaaccc tgcatatgaa attggtgata tatacgaaga agatgtaaca 300
320 cctaaagatt ttggtcgtgt aggtgctcaa gcagcgaaac aagcagtaat gcaacgtctt 360
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326 actgtaattg ttaaatcagt agcacgtgaa gctggcgatc gctctaaaat tagtgtcttc 720
327 tctgaaaaca atgatataga tgctgttggt gcatgtgttg gtgctaaagg cgcacgtggt 780
328 gaagctgttg ttgaagagct agtggtgtaa aaaatcgaca tcgttcaatg gaatgaagat 840
329 ccaaaagtat ttgtaaaaaa tgctttaagc ctttctcaag ttttagaagt tattgttgat 900

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VERIFICATION SUMMARY

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Input Set : A:\pb560-sl.txt

Output Set: N:\CRF3\08162001\I925637.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:2102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52

L:2340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58

L:2655 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65

L:2722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66

L:2761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68